



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Pulst, Stefan M.
- (ii) TITLE OF INVENTION: NUCLEIC ACID ENCODING SPINOCEREBELLAR  
ATAXIA-2 AND PRODUCTS RELATED THERETO
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Pretty, Schroeder & Poplawski
  - (B) STREET: 444 South Flower Street, Suite 2000
  - (C) CITY: Los Angeles
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 90071
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: 3.5" diskette
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/727,084
  - (B) FILING DATE: October 8, 1996
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Viviana Amzel, Ph. D.
  - (B) REGISTRATION NUMBER: 30930
  - (C) REFERENCE/DOCKET NUMBER: P07 37217
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 213-622-7700
  - (B) TELEFAX: 213-489-4210

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 516 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TTGGTAGCAA CGGAAACGGC GCGGCGCGCT TTCGGCCCGG CTCCCGGCGG CTCCTTGGTC      60
TCGGCGGGCC TCCCCGCCCC TTCGTCGTCG TCCTTCTCCC CCTCGCCAGC CCGGGCGCCC      120
CTCCGGCCGC GCCAACCCGC GCCTCCCCGC TCGGCGCCCG TCGTCCCCG CCGCGTTCCG      180
GCGTCTCCTT GCGCGGCCCC GCTCCCGGCT GTCCCCGCC GCGGTGCGAG CCGGTGTATG      240
GGCCCCTCAC CATGTCGCTG AAGCCCCAGC AGCAGCAGCA GCAGCAGCAG CAACAGCAGC      300
AGCAGCAACA GCAGCAGCAG CAGCAGCAGC AGCCGCCGCC CGCGGCTGCC AATGTCCGCA      360
AGCCCGGCGG CAGCGGCCTT CTAGCGTCGC CCGCCGCCGC GCCTTCGCCG TCCTCGTCCT      420
CGGTCTCCTC GTCCTCGGCC ACGGCTCCCT CCTCGGTGGT CGCGGCGACC TCCGGCGGCG      480
GGAGGCCCGG CTTGGGCAGG TGGGTGTCGG CACCCC                                516
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 163..4101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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ACCCCCGAGA AAGCAACCCA GCGCGCCGCC CGCTCCTCAC GTGTCCCTCC CGGCCCCGGG      60
GCCACCTCAC GTTCTGCTTC CGTCTGACCC CTCCGACTTC CGGTAAAGAG TCCCTATCCG      120
CACCTCCGCT CCCACCCGGC GCCTCGGCGC GCCCGCCCTC CG ATG CGC TCA GCG      174
                                   Met Arg Ser Ala
                                   1
GCC GCA GCT CCT CGG AGT CCC GCG GTG GCC ACC GAG TCT CGC CGC TTC      222
Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu Ser Arg Arg Phe
  5              10              15              20
GCC GCA GCC AGG TGG CCC GGG TGG CGC TCG CTC CAG CGG CCG GCG CGG      270
Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln Arg Pro Ala Arg
  25              30              35
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CGG AGC GGG CGG GGC GGC GGT GGC GCG GCC CCG GGA CCG TAT CCC TCC	318
Arg Ser Gly Arg Gly Gly Gly Gly Ala Ala Pro Gly Pro Tyr Pro Ser	
40 45 50	
GCC GCC CCT CCC CCG CCC GGC CCC GGC CCC CCT CCC TCC CGG CAG AGC	366
Ala Ala Pro Pro Pro Pro Gly Pro Gly Pro Pro Pro Ser Arg Gln Ser	
55 60 65	
TCG CCT CCC TCC GCC TCA GAC TGT TTT GGT AGC AAC GGC AAC GGC GGC	414
Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn Gly Asn Gly Gly	
70 75 80	
GGC GCG TTT CGG CCC GGC TCC CGG CGG CTC CTT GGT CTC GGC GGG CCT	462
Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly Leu Gly Gly Pro	
85 90 95 100	
CCC CGC CCC TTC GTC GTC GTC CTT CTC CCC CTC GCC AGC CCG GGC GCC	510
Pro Arg Pro Phe Val Val Val Leu Leu Pro Leu Ala Ser Pro Gly Ala	
105 110 115	
CCT CCG GCC GCG CCA ACC CGC GCC TCC CCG CTC GGC GCC CGT GCG TCC	558
Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly Ala Arg Ala Ser	
120 125 130	
CCG CCG CGT TCC GGC GTC TCC TTG GCG CGC CCG GCT CCC GGC TGT CCC	606
Pro Pro Arg Ser Gly Val Ser Leu Ala Arg Pro Ala Pro Gly Cys Pro	
135 140 145	
CGC CCG GCG TGC GAG CCG GTG TAT GGG CCC CTC ACC ATG TCG CTG AAG	654
Arg Pro Ala Cys Glu Pro Val Tyr Gly Pro Leu Thr Met Ser Leu Lys	
150 155 160	
CCC CAG CAG CAG CAG CAG CAG CAG CAG CAA CAG CAG CAG CAG CAA CAG	702
Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln	
165 170 175 180	
CAG CAG CAG CAG CAG CAG CAG CCG CCG CCC GCG GCT GCC AAT GTC CGC	750
Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro Ala Ala Ala Asn Val Arg	
185 190 195	
AAG CCC GGC GGC AGC GGC CTT CTA GCG TCG CCC GCC GCC GCG CCT TCG	798
Lys Pro Gly Gly Ser Gly Leu Leu Ala Ser Pro Ala Ala Ala Pro Ser	
200 205 210	
CCG TCC TCG TCC TCG GTC TCC TCG TCC TCG GCC ACG GCT CCC TCC TCG	846
Pro Ser Ser Ser Ser Val Ser Ser Ser Ser Ala Thr Ala Pro Ser Ser	
215 220 225	
GTG GTC GCG GCG ACC TCC GGC GGC GGG AGG CCC GGC CTG GGC AGA GGT	894
Val Val Ala Ala Thr Ser Gly Gly Gly Arg Pro Gly Leu Gly Arg Gly	
230 235 240	
CGA AAC AGT AAC AAA GGA CTG CCT CAG TCT ACG ATT TCT TTT GAT GGA	942
Arg Asn Ser Asn Lys Gly Leu Pro Gln Ser Thr Ile Ser Phe Asp Gly	

245	250	255	260	
ATC TAT GCA AAT ATG AGG ATG GTT CAT ATA CTT ACA TCA GTT GTT GGC				990
Ile Tyr Ala Asn Met Arg Met Val His Ile Leu Thr Ser Val Val Gly	265	270	275	
TCC AAA TGT GAA GTA CAA GTG AAA AAT GGA GGT ATA TAT GAA GGA GTT				1038
Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile Tyr Glu Gly Val	280	285	290	
TTT AAA ACT TAC AGT CCG AAG TGT GAT TTG GTA CTT GAT GCC GCA CAT				1086
Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu Asp Ala Ala His	295	300	305	
GAG AAA AGT ACA GAA TCC AGT TCG GGG CCG AAA CGT GAA GAA ATA ATG				1134
Glu Lys Ser Thr Glu Ser Ser Ser Gly Pro Lys Arg Glu Glu Ile Met	310	315	320	
GAG AGT ATT TTG TTC AAA TGT TCA GAC TTT GTT GTG GTA CAG TTT AAA				1182
Glu Ser Ile Leu Phe Lys Cys Ser Asp Phe Val Val Val Gln Phe Lys	325	330	335	340
GAT ATG GAC TCC AGT TAT GCA AAA AGA GAT GCT TTT ACT GAC TCT GCT				1230
Asp Met Asp Ser Ser Tyr Ala Lys Arg Asp Ala Phe Thr Asp Ser Ala	345	350	355	
ATC AGT GCT AAA GTG AAT GGC GAA CAC AAA GAG AAG GAC CTG GAG CCC				1278
Ile Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys Asp Leu Glu Pro	360	365	370	
TGG GAT GCA GGT GAA CTC ACA GCC AAT GAG GAA CTT GAG GCT TTG GAA				1326
Trp Asp Ala Gly Glu Leu Thr Ala Asn Glu Glu Leu Glu Ala Leu Glu	375	380	385	
AAT GAC GTA TCT AAT GGA TGG GAT CCC AAT GAT ATG TTT CGA TAT AAT				1374
Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met Phe Arg Tyr Asn	390	395	400	
GAA GAA AAT TAT GGT GTA GTG TCT ACG TAT GAT AGC AGT TTA TCT TCG				1422
Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser Ser Leu Ser Ser	405	410	415	420
TAT ACA GTG CCC TTA GAA AGA GAT AAC TCA GAA GAA TTT TTA AAA CGG				1470
Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu Phe Leu Lys Arg	425	430	435	
GAA GCA AGG GCA AAC CAG TTA GCA GAA GAA ATT GAG TCA AGT GCC CAG				1518
Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu Ser Ser Ala Gln	440	445	450	
TAC AAA GCT CGA GTG GCC CTG GAA AAT GAT GAT AGG AGT GAG GAA GAA				1566
Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp Asp Arg Ser Glu Glu Glu	455	460	465	

AAA TAC ACA GCA GTT CAG AGA AAT TCC AGT GAA CGT GAG GGG CAC AGC	1614
Lys Tyr Thr Ala Val Gln Arg Asn Ser Ser Glu Arg Glu Gly His Ser	
470 475 480	
ATA AAC ACT AGG GAA AAT AAA TAT ATT CCT CCT GGA CAA AGA AAT AGA	1662
Ile Asn Thr Arg Glu Asn Lys Tyr Ile Pro Pro Gly Gln Arg Asn Arg	
485 490 495 500	
GAA GTC ATA TCC TGG GGA AGT GGG AGA CAG AAT TCA CCG CGT ATG GGC	1710
Glu Val Ile Ser Trp Gly Ser Gly Arg Gln Asn Ser Pro Arg Met Gly	
505 510 515	
CAG CCT GGA TCG GGC TCC ATG CCA TCA AGA TCC ACT TCT CAC ACT TCA	1758
Gln Pro Gly Ser Gly Ser Met Pro Ser Arg Ser Thr Ser His Thr Ser	
520 525 530	
GAT TTC AAC CCG AAT TCT GGT TCA GAC CAA AGA GTA GTT AAT GGA GGT	1806
Asp Phe Asn Pro Asn Ser Gly Ser Asp Gln Arg Val Val Asn Gly Gly	
535 540 545	
GTT CCC TGG CCA TCG CCT TGC CCA TCT CCT TCC TCT CGC CCA CCT TCT	1854
Val Pro Trp Pro Ser Pro Cys Pro Ser Pro Ser Ser Arg Pro Pro Ser	
550 555 560	
CGC TAC CAG TCA GGT CCC AAC TCT CTT CCA CCT CGG GCA GCC ACC CCT	1902
Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg Ala Ala Thr Pro	
565 570 575 580	
ACA CGG CCG CCC TCC AGG CCC CCC TCG CGG CCA TCC AGA CCC CCG TCT	1950
Thr Arg Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser Arg Pro Pro Ser	
585 590 595	
CAC CCC TCT GCT CAT GGT TCT CCA GCT CCT GTC TCT ACT ATG CCT AAA	1998
His Pro Ser Ala His Gly Ser Pro Ala Pro Val Ser Thr Met Pro Lys	
600 605 610	
CGC ATG TCT TCA GAA GGG CCT CCA AGG ATG TCC CCA AAG GCC CAG CGA	2046
Arg Met Ser Ser Glu Gly Pro Pro Arg Met Ser Pro Lys Ala Gln Arg	
615 620 625	
CAT CCT CGA AAT CAC AGA GTT TCT GCT GGG AGG GGT TCC ATA TCC AGT	2094
His Pro Arg Asn His Arg Val Ser Ala Gly Arg Gly Ser Ile Ser Ser	
630 635 640	
GGC CTA GAA TTT GTA TCC CAC AAC CCA CCC AGT GAA GCA GCT ACT CCT	2142
Gly Leu Glu Phe Val Ser His Asn Pro Pro Ser Glu Ala Ala Thr Pro	
645 650 655 660	
CCA GTA GCA AGG ACC AGT CCC TCG GGG GGA ACG TGG TCA TCA GTG GTC	2190
Pro Val Ala Arg Thr Ser Pro Ser Gly Gly Thr Trp Ser Ser Val Val	
665 670 675	
AGT GGG GTT CCA AGA TTA TCC CCT AAA ACT CAT AGA CCC AGG TCT CCC	2238
Ser Gly Val Pro Arg Leu Ser Pro Lys Thr His Arg Pro Arg Ser Pro	

680										685					690					
AGA	CAG	AAC	AGT	ATT	GGA	AAT	ACC	CCC	AGT	GGG	CCA	GTT	CTT	GCT	TCT		2286			
Arg	Gln	Asn	Ser	Ile	Gly	Asn	Thr	Pro	Ser	Gly	Pro	Val	Leu	Ala	Ser					
		695					700					705								
CCC	CAA	GCT	GGT	ATT	ATT	CCA	ACT	GAA	GCT	GTT	GCC	ATG	CCT	ATT	CCA		2334			
Pro	Gln	Ala	Gly	Ile	Ile	Pro	Thr	Glu	Ala	Val	Ala	Met	Pro	Ile	Pro					
		710				715					720									
GCT	GCA	TCT	CCT	ACG	CCT	GCT	AGT	CCT	GCA	TCG	AAC	AGA	GCT	GTT	ACC		2382			
Ala	Ala	Ser	Pro	Thr	Pro	Ala	Ser	Pro	Ala	Ser	Asn	Arg	Ala	Val	Thr					
		725			730				735					740						
CCT	TCT	AGT	GAG	GCT	AAA	GAT	TCC	AGG	CTT	CAA	GAT	CAG	AGG	CAG	AAC		2430			
Pro	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Arg	Leu	Gln	Asp	Gln	Arg	Gln	Asn					
			745					750				755								
TCT	CCT	GCA	GGG	AAT	AAA	GAA	AAT	ATT	AAA	CCC	AAT	GAA	ACA	TCA	CCT		2478			
Ser	Pro	Ala	Gly	Asn	Lys	Glu	Asn	Ile	Lys	Pro	Asn	Glu	Thr	Ser	Pro					
			760					765				770								
AGC	TTC	TCA	AAA	GCT	GAA	AAC	AAA	GGT	ATA	TCA	CCA	GTT	GTT	TCT	GAA		2526			
Ser	Phe	Ser	Lys	Ala	Glu	Asn	Lys	Gly	Ile	Ser	Pro	Val	Val	Ser	Glu					
		775					780					785								
CAT	AGA	AAA	CAG	ATT	GAT	GAT	TTA	AAG	AAA	TTT	AAG	AAT	GAT	TTT	AGG		2574			
His	Arg	Lys	Gln	Ile	Asp	Asp	Leu	Lys	Lys	Phe	Lys	Asn	Asp	Phe	Arg					
		790				795					800									
TTA	CAG	CCA	AGT	TCT	ACT	TCT	GAA	TCT	ATG	GAT	CAA	CTA	CTA	AAC	AAA		2622			
Leu	Gln	Pro	Ser	Ser	Thr	Ser	Glu	Ser	Met	Asp	Gln	Leu	Leu	Asn	Lys					
		805			810				815					820						
AAT	AGA	GAG	GGA	GAA	AAA	TCA	AGA	GAT	TTG	ATC	AAA	GAC	AAA	ATT	GAA		2670			
Asn	Arg	Glu	Gly	Glu	Lys	Ser	Arg	Asp	Leu	Ile	Lys	Asp	Lys	Ile	Glu					
			825					830				835								
CCA	AGT	GCT	AAG	GAT	TCT	TTC	ATT	GAA	AAT	AGC	AGC	AGC	AAC	TGT	ACC		2718			
Pro	Ser	Ala	Lys	Asp	Ser	Phe	Ile	Glu	Asn	Ser	Ser	Ser	Asn	Cys	Thr					
		840						845				850								
AGT	GGC	AGC	AGC	AAG	CCG	AAT	AGC	CCC	AGC	ATT	TCC	CCT	TCA	ATA	CTT		2766			
Ser	Gly	Ser	Ser	Lys	Pro	Asn	Ser	Pro	Ser	Ile	Ser	Pro	Ser	Ile	Leu					
		855					860					865								
AGT	AAC	ACG	GAG	CAC	AAG	AGG	GGA	CCT	GAG	GTC	ACT	TCC	CAA	GGG	GTT		2814			
Ser	Asn	Thr	Glu	His	Lys	Arg	Gly	Pro	Glu	Val	Thr	Ser	Gln	Gly	Val					
		870				875					880									
CAG	ACT	TCC	AGC	CCA	GCA	TGT	AAA	CAA	GAG	AAA	GAC	GAT	AAG	GAA	GAG		2862			
Gln	Thr	Ser	Ser	Pro	Ala	Cys	Lys	Gln	Glu	Lys	Asp	Asp	Lys	Glu	Glu					
		885			890				895					900						

AAG AAA GAC GCA GCT GAG CAA GTT AGG AAA TCA ACA TTG AAT CCC AAT	2910
Lys Lys Asp Ala Ala Glu Gln Val Arg Lys Ser Thr Leu Asn Pro Asn	
905 910 915	
GCA AAG GAG TTC AAC CCA CGT TCC TTC TCT CAG CCA AAG CCT TCT ACT	2958
Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro Lys Pro Ser Thr	
920 925 930	
ACC CCA ACT TCA CCT CGG CCT CAA GCA CAA CCT AGC CCA TCT ATG GTG	3006
Thr Pro Thr Ser Pro Arg Pro Gln Ala Gln Pro Ser Pro Ser Met Val	
935 940 945	
GGT CAT CAA CAG CCA ACT CCA GTT TAT ACT CAG CCT GTT TGT TTT GCA	3054
Gly His Gln Gln Pro Thr Pro Val Tyr Thr Gln Pro Val Cys Phe Ala	
950 955 960	
CCA AAT ATG ATG TAT CCA GTC CCA GTG AGC CCA GGC GTG CAA CCT TTA	3102
Pro Asn Met Met Tyr Pro Val Pro Val Ser Pro Gly Val Gln Pro Leu	
965 970 975 980	
TAC CCA ATA CCT ATG ACG CCC ATG CCA GTG AAT CAA GCC AAG ACA TAT	3150
Tyr Pro Ile Pro Met Thr Pro Met Pro Val Asn Gln Ala Lys Thr Tyr	
985 990 995	
AGA GCA GTA CCA AAT ATG CCC CAA CAG CGG CAA GAC CAG CAT CAT CAG	3198
Arg Ala Val Pro Asn Met Pro Gln Gln Arg Gln Asp Gln His His Gln	
1000 1005 1010	
AGT GCC ATG ATG CAC CCA GCG TCA GCA GCG GGC CCA CCG ATT GCA GCC	3246
Ser Ala Met Met His Pro Ala Ser Ala Ala Gly Pro Pro Ile Ala Ala	
1015 1020 1025	
ACC CCA CCA GCT TAC TCC ACG CAA TAT GTT GCC TAC AGT CCT CAG CAG	3294
Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val Ala Tyr Ser Pro Gln Gln	
1030 1035 1040	
TTC CCA AAT CAG CCC CTT GTT CAG CAT GTG CCA CAT TAT CAG TCT CAG	3342
Phe Pro Asn Gln Pro Leu Val Gln His Val Pro His Tyr Gln Ser Gln	
1045 1050 1055 1060	
CAT CCT CAT GTC TAT AGT CCT GTA ATA CAG GGT AAT GCT AGA ATG ATG	3390
His Pro His Val Tyr Ser Pro Val Ile Gln Gly Asn Ala Arg Met Met	
1065 1070 1075	
GCA CCA CCA ACA CAC GCC CAG CCT GGT TTA GTA TCT TCT TCA GCA ACT	3438
Ala Pro Pro Thr His Ala Gln Pro Gly Leu Val Ser Ser Ser Ala Thr	
1080 1085 1090	
CAG TAC GGG GCT CAT GAG CAG ACG CAT GCG ATG TAT GCA TGT CCC AAA	3486
Gln Tyr Gly Ala His Glu Gln Thr His Ala Met Tyr Ala Cys Pro Lys	
1095 1100 1105	
TTA CCA TAC AAC AAG GAG ACA AGC CCT TCT TTC TAC TTT GCC ATT TCC	3534
Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe Tyr Phe Ala Ile Ser	

1110	1115	1120	
ACG GGC TCC CTT GCT CAG CAG TAT GCG CAC CCT AAC GCT ACC CTG CAC			3582
Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro Asn Ala Thr Leu His			
1125	1130	1135	1140
CCA CAT ACT CCA CAC CCT CAG CCT TCA GCT ACC CCC ACT GGA CAG CAG			3630
Pro His Thr Pro His Pro Gln Pro Ser Ala Thr Pro Thr Gly Gln Gln			
1145	1150	1155	
CAA AGC CAA CAT GGT GGA AGT CAT CCT GCA CCC AGT CCT GTT CAG CAC			3678
Gln Ser Gln His Gly Gly Ser His Pro Ala Pro Ser Pro Val Gln His			
1160	1165	1170	
CAT CAG CAC CAG GCC GCC CAG GCT CTC CAT CTG GCC AGT CCA CAG CAG			3726
His Gln His Gln Ala Ala Gln Ala Leu His Leu Ala Ser Pro Gln Gln			
1175	1180	1185	
CAG TCA GCC ATT TAC CAC GCG GGG CTT GCG CCA ACT CCA CCC TCC ATG			3774
Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro Thr Pro Pro Ser Met			
1190	1195	1200	
ACA CCT GCC TCC AAC ACG CAG TCG CCA CAG AAT AGT TTC CCA GCA GCA			3822
Thr Pro Ala Ser Asn Thr Gln Ser Pro Gln Asn Ser Phe Pro Ala Ala			
1205	1210	1215	1220
CAA CAG ACT GTC TTT ACG ATC CAT CCT TCT CAC GTT CAG CCG GCG TAT			3870
Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val Gln Pro Ala Tyr			
1225	1230	1235	
ACC AAC CCA CCC CAC ATG GCC CAC GTA CCT CAG GCT CAT GTA CAG TCA			3918
Thr Asn Pro Pro His Met Ala His Val Pro Gln Ala His Val Gln Ser			
1240	1245	1250	
GGA ATG GTT CCT TCT CAT CCA ACT GCC CAT GCG CCA ATG ATG CTA ATG			3966
Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro Met Met Leu Met			
1255	1260	1265	
ACG ACA CAG CCA CCC GGC GGT CCC CAG GCC GCC CTC GCT CAA AGT GCA			4014
Thr Thr Gln Pro Pro Gly Gly Pro Gln Ala Ala Leu Ala Gln Ser Ala			
1270	1275	1280	
CTA CAG CCC ATT CCA GTC TCG ACA ACA GCG CAT TTC CCC TAT ATG ACG			4062
Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe Pro Tyr Met Thr			
1285	1290	1295	1300
CAC CCT TCA GTA CAA GCC CAC CAC CAA CAG CAG TTG TAAGGCTGCC			4108
His Pro Ser Val Gln Ala His His Gln Gln Gln Leu			
1305	1310		
CTGGAGGAAC CGAAAGGCCA AATCCCTCC TCCCTTCTAC TGCTTCTACC AACTGGAAGC			4168
ACAGAAAACT AGAATTTCAT TTATTTTGTT TTAAATAT ATATGTTGAT TTCTTGTAAC			4228



ATCCAATAGG AATGCTAACA GTTCACTTGC AGTGGAAGAT ACTTGGACCG AGTAGAGGCA	4288
TTTAGGAACT TGGGGGCTAT TCCATAATTC CATATGCTGT TTCAGAGTCC CGCAGGTACC	4348
CCAGCTCTGC TTGCCGAAAC TGGAAGTTAT TTATTTTTTA ATAACCCTTG AAAGTCATGA	4408
ACACATCAGC TAGCAAAAGA AGTAACAAGA GTGATTCTTG CTGCTATTAC TGCTAAAAAA	4468
AAAAAAAAAA AAA	4481

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1312 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Arg	Ser	Ala	Ala	Ala	Ala	Pro	Arg	Ser	Pro	Ala	Val	Ala	Thr	Glu	1	5	10	15
Ser	Arg	Arg	Phe	Ala	Ala	Ala	Arg	Trp	Pro	Gly	Trp	Arg	Ser	Leu	Gln	20	25	30	
Arg	Pro	Ala	Arg	Arg	Ser	Gly	Arg	Gly	Gly	Gly	Gly	Ala	Ala	Pro	Gly	35	40	45	
Pro	Tyr	Pro	Ser	Ala	Ala	Pro	Pro	Pro	Pro	Gly	Pro	Gly	Pro	Pro	Pro	50	55	60	
Ser	Arg	Gln	Ser	Ser	Pro	Pro	Ser	Ala	Ser	Asp	Cys	Phe	Gly	Ser	Asn	65	70	75	80
Gly	Asn	Gly	Gly	Gly	Ala	Phe	Arg	Pro	Gly	Ser	Arg	Arg	Leu	Leu	Gly	85	90	95	
Leu	Gly	Gly	Pro	Pro	Arg	Pro	Phe	Val	Val	Val	Leu	Leu	Pro	Leu	Ala	100	105	110	
Ser	Pro	Gly	Ala	Pro	Pro	Ala	Ala	Pro	Thr	Arg	Ala	Ser	Pro	Leu	Gly	115	120	125	
Ala	Arg	Ala	Ser	Pro	Pro	Arg	Ser	Gly	Val	Ser	Leu	Ala	Arg	Pro	Ala	130	135	140	
Pro	Gly	Cys	Pro	Arg	Pro	Ala	Cys	Glu	Pro	Val	Tyr	Gly	Pro	Leu	Thr	145	150	155	160
Met	Ser	Leu	Lys	Pro	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	165	170	175	

Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Pro	Pro	Pro	Ala	Ala	
			180						185					190			
Ala	Asn	Val	Arg	Lys	Pro	Gly	Gly	Ser	Gly	Leu	Leu	Ala	Ser	Pro	Ala		
		195					200					205					
Ala	Ala	Pro	Ser	Pro	Ser	Ser	Ser	Ser	Val	Ser	Ser	Ser	Ser	Ala	Thr		
		210				215					220						
Ala	Pro	Ser	Ser	Val	Val	Ala	Ala	Thr	Ser	Gly	Gly	Gly	Arg	Pro	Gly		
225					230					235					240		
Leu	Gly	Arg	Gly	Arg	Asn	Ser	Asn	Lys	Gly	Leu	Pro	Gln	Ser	Thr	Ile		
				245					250					255			
Ser	Phe	Asp	Gly	Ile	Tyr	Ala	Asn	Met	Arg	Met	Val	His	Ile	Leu	Thr		
		260						265					270				
Ser	Val	Val	Gly	Ser	Lys	Cys	Glu	Val	Gln	Val	Lys	Asn	Gly	Gly	Ile		
		275					280					285					
Tyr	Glu	Gly	Val	Phe	Lys	Thr	Tyr	Ser	Pro	Lys	Cys	Asp	Leu	Val	Leu		
	290					295					300						
Asp	Ala	Ala	His	Glu	Lys	Ser	Thr	Glu	Ser	Ser	Ser	Gly	Pro	Lys	Arg		
305					310					315					320		
Glu	Glu	Ile	Met	Glu	Ser	Ile	Leu	Phe	Lys	Cys	Ser	Asp	Phe	Val	Val		
				325					330					335			
Val	Gln	Phe	Lys	Asp	Met	Asp	Ser	Ser	Tyr	Ala	Lys	Arg	Asp	Ala	Phe		
			340					345					350				
Thr	Asp	Ser	Ala	Ile	Ser	Ala	Lys	Val	Asn	Gly	Glu	His	Lys	Glu	Lys		
	355						360					365					
Asp	Leu	Glu	Pro	Trp	Asp	Ala	Gly	Glu	Leu	Thr	Ala	Asn	Glu	Glu	Leu		
	370					375					380						
Glu	Ala	Leu	Glu	Asn	Asp	Val	Ser	Asn	Gly	Trp	Asp	Pro	Asn	Asp	Met		
385					390					395					400		
Phe	Arg	Tyr	Asn	Glu	Glu	Asn	Tyr	Gly	Val	Val	Ser	Thr	Tyr	Asp	Ser		
			405						410					415			
Ser	Leu	Ser	Ser	Tyr	Thr	Val	Pro	Leu	Glu	Arg	Asp	Asn	Ser	Glu	Glu		
			420					425					430				
Phe	Leu	Lys	Arg	Glu	Ala	Arg	Ala	Asn	Gln	Leu	Ala	Glu	Glu	Ile	Glu		
		435					440					445					
Ser	Ser	Ala	Gln	Tyr	Lys	Ala	Arg	Val	Ala	Leu	Glu	Asn	Asp	Asp	Arg		
	450					455					460						

Ser Glu Glu Glu Lys Tyr Thr Ala Val Gln Arg Asn Ser Ser Glu Arg  
 465 470 475 480

Glu Gly His Ser Ile Asn Thr Arg Glu Asn Lys Tyr Ile Pro Pro Gly  
 485 490 495

Gln Arg Asn Arg Glu Val Ile Ser Trp Gly Ser Gly Arg Gln Asn Ser  
 500 505 510

Pro Arg Met Gly Gln Pro Gly Ser Gly Ser Met Pro Ser Arg Ser Thr  
 515 520 525

Ser His Thr Ser Asp Phe Asn Pro Asn Ser Gly Ser Asp Gln Arg Val  
 530 535 540

Val Asn Gly Gly Val Pro Trp Pro Ser Pro Cys Pro Ser Pro Ser Ser  
 545 550 555 560

Arg Pro Pro Ser Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg  
 565 570 575

Ala Ala Thr Pro Thr Arg Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser  
 580 585 590

Arg Pro Pro Ser His Pro Ser Ala His Gly Ser Pro Ala Pro Val Ser  
 595 600 605

Thr Met Pro Lys Arg Met Ser Ser Glu Gly Pro Pro Arg Met Ser Pro  
 610 615 620

Lys Ala Gln Arg His Pro Arg Asn His Arg Val Ser Ala Gly Arg Gly  
 625 630 635 640

Ser Ile Ser Ser Gly Leu Glu Phe Val Ser His Asn Pro Pro Ser Glu  
 645 650 655

Ala Ala Thr Pro Pro Val Ala Arg Thr Ser Pro Ser Gly Gly Thr Trp  
 660 665 670

Ser Ser Val Val Ser Gly Val Pro Arg Leu Ser Pro Lys Thr His Arg  
 675 680 685

Pro Arg Ser Pro Arg Gln Asn Ser Ile Gly Asn Thr Pro Ser Gly Pro  
 690 695 700

Val Leu Ala Ser Pro Gln Ala Gly Ile Ile Pro Thr Glu Ala Val Ala  
 705 710 715 720

Met Pro Ile Pro Ala Ala Ser Pro Thr Pro Ala Ser Pro Ala Ser Asn  
 725 730 735

Arg Ala Val Thr Pro Ser Ser Glu Ala Lys Asp Ser Arg Leu Gln Asp  
 740 745 750

Gln	Arg	Gln	Asn	Ser	Pro	Ala	Gly	Asn	Lys	Glu	Asn	Ile	Lys	Pro	Asn
		755					760					765			
Glu	Thr	Ser	Pro	Ser	Phe	Ser	Lys	Ala	Glu	Asn	Lys	Gly	Ile	Ser	Pro
	770					775					780				
Val	Val	Ser	Glu	His	Arg	Lys	Gln	Ile	Asp	Asp	Leu	Lys	Lys	Phe	Lys
785					790					795					800
Asn	Asp	Phe	Arg	Leu	Gln	Pro	Ser	Ser	Thr	Ser	Glu	Ser	Met	Asp	Gln
				805					810					815	
Leu	Leu	Asn	Lys	Asn	Arg	Glu	Gly	Glu	Lys	Ser	Arg	Asp	Leu	Ile	Lys
			820					825					830		
Asp	Lys	Ile	Glu	Pro	Ser	Ala	Lys	Asp	Ser	Phe	Ile	Glu	Asn	Ser	Ser
		835					840					845			
Ser	Asn	Cys	Thr	Ser	Gly	Ser	Ser	Lys	Pro	Asn	Ser	Pro	Ser	Ile	Ser
	850					855					860				
Pro	Ser	Ile	Leu	Ser	Asn	Thr	Glu	His	Lys	Arg	Gly	Pro	Glu	Val	Thr
865					870					875					880
Ser	Gln	Gly	Val	Gln	Thr	Ser	Ser	Pro	Ala	Cys	Lys	Gln	Glu	Lys	Asp
				885					890					895	
Asp	Lys	Glu	Glu	Lys	Lys	Asp	Ala	Ala	Glu	Gln	Val	Arg	Lys	Ser	Thr
		900						905					910		
Leu	Asn	Pro	Asn	Ala	Lys	Glu	Phe	Asn	Pro	Arg	Ser	Phe	Ser	Gln	Pro
		915					920					925			
Lys	Pro	Ser	Thr	Thr	Pro	Thr	Ser	Pro	Arg	Pro	Gln	Ala	Gln	Pro	Ser
	930					935					940				
Pro	Ser	Met	Val	Gly	His	Gln	Gln	Pro	Thr	Pro	Val	Tyr	Thr	Gln	Pro
945					950					955					960
Val	Cys	Phe	Ala	Pro	Asn	Met	Met	Tyr	Pro	Val	Pro	Val	Ser	Pro	Gly
				965					970					975	
Val	Gln	Pro	Leu	Tyr	Pro	Ile	Pro	Met	Thr	Pro	Met	Pro	Val	Asn	Gln
			980					985					990		
Ala	Lys	Thr	Tyr	Arg	Ala	Val	Pro	Asn	Met	Pro	Gln	Gln	Arg	Gln	Asp
		995					1000					1005			
Gln	His	His	Gln	Ser	Ala	Met	Met	His	Pro	Ala	Ser	Ala	Ala	Gly	Pro
	1010					1015					1020				
Pro	Ile	Ala	Ala	Thr	Pro	Pro	Ala	Tyr	Ser	Thr	Gln	Tyr	Val	Ala	Tyr
1025					1030						1035				1040

Ser Pro Gln Gln Phe Pro Asn Gln Pro Leu Val Gln His Val Pro His  
 1045 1050 1055  
 Tyr Gln Ser Gln His Pro His Val Tyr Ser Pro Val Ile Gln Gly Asn  
 1060 1065 1070  
 Ala Arg Met Met Ala Pro Pro Thr His Ala Gln Pro Gly Leu Val Ser  
 1075 1080 1085  
 Ser Ser Ala Thr Gln Tyr Gly Ala His Glu Gln Thr His Ala Met Tyr  
 1090 1095 1100  
 Ala Cys Pro Lys Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe Tyr  
 1105 1110 1115 1120  
 Phe Ala Ile Ser Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro Asn  
 1125 1130 1135  
 Ala Thr Leu His Pro His Thr Pro His Pro Gln Pro Ser Ala Thr Pro  
 1140 1145 1150  
 Thr Gly Gln Gln Gln Ser Gln His Gly Gly Ser His Pro Ala Pro Ser  
 1155 1160 1165  
 Pro Val Gln His His Gln His Gln Ala Ala Gln Ala Leu His Leu Ala  
 1170 1175 1180  
 Ser Pro Gln Gln Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro Thr  
 1185 1190 1195 1200  
 Pro Pro Ser Met Thr Pro Ala Ser Asn Thr Gln Ser Pro Gln Asn Ser  
 1205 1210 1215  
 Phe Pro Ala Ala Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val  
 1220 1225 1230  
 Gln Pro Ala Tyr Thr Asn Pro Pro His Met Ala His Val Pro Gln Ala  
 1235 1240 1245  
 His Val Gln Ser Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro  
 1250 1255 1260  
 Met Met Leu Met Thr Thr Gln Pro Pro Gly Gly Pro Gln Ala Ala Leu  
 1265 1270 1275 1280  
 Ala Gln Ser Ala Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe  
 1285 1290 1295  
 Pro Tyr Met Thr His Pro Ser Val Gln Ala His His Gln Gln Gln Leu  
 1300 1305 1310

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..1255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

G CAC GAG GGG CCG CTC ACC ATG TCG CTG AAG CCG CAG CCG CAG CCG	46
His Glu Gly Pro Leu Thr Met Ser Leu Lys Pro Gln Pro Gln Pro	
1 5 10 15	
CCC GCG CCC GCC ACT GGC CGC AAG CCC GGC GGC GGC CTG CTC TCG TCG	94
Pro Ala Pro Ala Thr Gly Arg Lys Pro Gly Gly Gly Leu Leu Ser Ser	
20 25 30	
CCC GGC GCC GCG CCG GCC TCG GCC GCG GTG ACC TCG GCT TCC GTG GTG	142
Pro Gly Ala Ala Pro Ala Ser Ala Ala Val Thr Ser Ala Ser Val Val	
35 40 45	
CCG GCC CCG GCC GCG CCG GTG GCG TCT TCC TCG GCG GCC GCG GGC GGC	190
Pro Ala Pro Ala Ala Pro Val Ala Ser Ser Ser Ala Ala Ala Gly Gly	
50 55 60	
GGG CGT CCC GGC CTG GGC AGA GGT CGG AAC AGT AGC AAA GGA CTG CCT	238
Gly Arg Pro Gly Leu Gly Arg Gly Arg Asn Ser Ser Lys Gly Leu Pro	
65 70 75	
CAG CCT ACG ATT TCT TTT GAT GGA ATC TAT GCA AAC GTG AGG ATG GTT	286
Gln Pro Thr Ile Ser Phe Asp Gly Ile Tyr Ala Asn Val Arg Met Val	
80 85 90 95	
CAT ATA CTT ACG TCA GTT GTT GGA TCG AAA TGT GAA GTA CAA GTG AAA	334
His Ile Leu Thr Ser Val Val Gly Ser Lys Cys Glu Val Gln Val Lys	
100 105 110	
AAC GGA GGC ATA TAT GAA GGA GTT TTT AAA ACA TAC AGT CCT AAG TGT	382
Asn Gly Gly Ile Tyr Glu Gly Val Phe Lys Thr Tyr Ser Pro Lys Cys	
115 120 125	
GAC TTG GTA CTT GAT GCT GCA CAT GAG AAA AGT ACA GAA TCC AGT TCG	430
Asp Leu Val Leu Asp Ala Ala His Glu Lys Ser Thr Glu Ser Ser Ser	

130	135	140	
GGG CCA AAA CGT GAA GAA ATA ATG GAG AGT GTT TTG TTC AAA TGC TCA			478
Gly Pro Lys Arg Glu Glu Ile Met Glu Ser Val Leu Phe Lys Cys Ser			
145	150	155	
GAC TTC GTT GTG GTA CAG TTT AAA GAT ACA GAC TCC AGT TAT GCA CGG			526
Asp Phe Val Val Val Gln Phe Lys Asp Thr Asp Ser Ser Tyr Ala Arg			
160	165	170	175
AGA GAT GCT TTT ACT GAC TCT GCT CTC AGC GCA AAG GTG AAT GGT GAG			574
Arg Asp Ala Phe Thr Asp Ser Ala Leu Ser Ala Lys Val Asn Gly Glu			
180	185	190	
CAC AAG GAG AAG GAC CTG GAG CCC TGG GAT GCA GGG GAG CTC ACG GCC			622
His Lys Glu Lys Asp Leu Glu Pro Trp Asp Ala Gly Glu Leu Thr Ala			
195	200	205	
AGC GAG GAG CTG GAG CTG GAG AAT GAT GTG TCT AAT GGA TGG GAC CCC			670
Ser Glu Glu Leu Glu Leu Glu Asn Asp Val Ser Asn Gly Trp Asp Pro			
210	215	220	
AAT GAC ATG TTT CGA TAT AAT GAA GAG AAT TAT GGT GTG GTG TCC ACA			718
Asn Asp Met Phe Arg Tyr Asn Glu Glu Asn Tyr Gly Val Val Ser Thr			
225	230	235	
TAT GAT AGC AGT TTA TCT TCA TAT ACG GTT CCT TTA GAA AGG GAC AAC			766
Tyr Asp Ser Ser Leu Ser Ser Tyr Thr Val Pro Leu Glu Arg Asp Asn			
240	245	250	255
TCA GAA GAA TTT CTT AAA CGG GAG GCA AGG GCA AAC CAG TTA GCA GAA			814
Ser Glu Glu Phe Leu Lys Arg Glu Ala Arg Ala Asn Gln Leu Ala Glu			
260	265	270	
GAA ATT GAA TCC AGT GCT CAG TAC AAA GCT CGT GTC GCC CTT GAG AAT			862
Glu Ile Glu Ser Ser Ala Gln Tyr Lys Ala Arg Val Ala Leu Glu Asn			
275	280	285	
GAT GAC CGG AGT GAG GAA GAA AAA TAC ACA GCA GTC CAG AGA AAC TGC			910
Asp Asp Arg Ser Glu Glu Glu Lys Tyr Thr Ala Val Gln Arg Asn Cys			
290	295	300	
AGT GAC CGG GAG GGG CAT GGC CCC AAC ACT AGG GAC AAT AAA TAT ATT			958
Ser Asp Arg Glu Gly His Gly Pro Asn Thr Arg Asp Asn Lys Tyr Ile			
305	310	315	
CCT CCT GGA CAA AGA AAC AGA GAA GTC CTA TCC TGG GGA AGT GGG AGA			1006
Pro Pro Gly Gln Arg Asn Arg Glu Val Leu Ser Trp Gly Ser Gly Arg			
320	325	330	335
CAG AGC TCA CCA CGG ATG GGC CAG CCT GGG CCA GGC TCC ATG CCG TCA			1054
Gln Ser Ser Pro Arg Met Gly Gln Pro Gly Pro Gly Ser Met Pro Ser			
340	345	350	

AGA GCT GCT TCT CAC ACT TCA GAT TTC AAC CCG AAC GCT GGC TCA GAC	1102
Arg Ala Ala Ser His Thr Ser Asp Phe Asn Pro Asn Ala Gly Ser Asp	
355 360 365	
CAA AGA GTA GTT AAT GGA GGT GTT CCC TGG CCA TCG CCT TGC CCA TCT	1150
Gln Arg Val Val Asn Gly Gly Val Pro Trp Pro Ser Pro Cys Pro Ser	
370 375 380	
CCT TCC TCT CGC CCA CCT TCT CGC TAC CAG TCA GGT CCC AAC TCT CTT	1198
Pro Ser Ser Arg Pro Pro Ser Arg Tyr Gln Ser Gly Pro Asn Ser Leu	
385 390 395	
CCA CCT CGG GCA GCC ACC CCT ACA CGG CCT CGT GCC GAA TTC CTG CAG	1246
Pro Pro Arg Ala Ala Thr Pro Thr Arg Pro Arg Ala Glu Phe Leu Gln	
400 405 410 415	
CCC GGG GAT CC	1257
Pro Gly Asp	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

His Glu Gly Pro Leu Thr Met Ser Leu Lys Pro Gln Pro Gln Pro Pro	
1 5 10 15	
Ala Pro Ala Thr Gly Arg Lys Pro Gly Gly Gly Leu Leu Ser Ser Pro	
20 25 30	
Gly Ala Ala Pro Ala Ser Ala Ala Val Thr Ser Ala Ser Val Val Pro	
35 40 45	
Ala Pro Ala Ala Pro Val Ala Ser Ser Ser Ala Ala Ala Gly Gly Gly	
50 55 60	
Arg Pro Gly Leu Gly Arg Gly Arg Asn Ser Ser Lys Gly Leu Pro Gln	
65 70 75 80	
Pro Thr Ile Ser Phe Asp Gly Ile Tyr Ala Asn Val Arg Met Val His	
85 90 95	
Ile Leu Thr Ser Val Val Gly Ser Lys Cys Glu Val Gln Val Lys Asn	
100 105 110	
Gly Gly Ile Tyr Glu Gly Val Phe Lys Thr Tyr Ser Pro Lys Cys Asp	



115							120							125	
Leu	Val	Leu	Asp	Ala	Ala	His	Glu	Lys	Ser	Thr	Glu	Ser	Ser	Ser	Gly
130						135					140				
Pro	Lys	Arg	Glu	Glu	Ile	Met	Glu	Ser	Val	Leu	Phe	Lys	Cys	Ser	Asp
145					150					155					160
Phe	Val	Val	Val	Gln	Phe	Lys	Asp	Thr	Asp	Ser	Ser	Tyr	Ala	Arg	Arg
				165					170					175	
Asp	Ala	Phe	Thr	Asp	Ser	Ala	Leu	Ser	Ala	Lys	Val	Asn	Gly	Glu	His
			180					185					190		
Lys	Glu	Lys	Asp	Leu	Glu	Pro	Trp	Asp	Ala	Gly	Glu	Leu	Thr	Ala	Ser
		195					200					205			
Glu	Glu	Leu	Glu	Leu	Glu	Asn	Asp	Val	Ser	Asn	Gly	Trp	Asp	Pro	Asn
	210					215					220				
Asp	Met	Phe	Arg	Tyr	Asn	Glu	Glu	Asn	Tyr	Gly	Val	Val	Ser	Thr	Tyr
225					230					235					240
Asp	Ser	Ser	Leu	Ser	Ser	Tyr	Thr	Val	Pro	Leu	Glu	Arg	Asp	Asn	Ser
			245						250					255	
Glu	Glu	Phe	Leu	Lys	Arg	Glu	Ala	Arg	Ala	Asn	Gln	Leu	Ala	Glu	Glu
			260					265					270		
Ile	Glu	Ser	Ser	Ala	Gln	Tyr	Lys	Ala	Arg	Val	Ala	Leu	Glu	Asn	Asp
	275						280					285			
Asp	Arg	Ser	Glu	Glu	Glu	Lys	Tyr	Thr	Ala	Val	Gln	Arg	Asn	Cys	Ser
	290					295					300				
Asp	Arg	Glu	Gly	His	Gly	Pro	Asn	Thr	Arg	Asp	Asn	Lys	Tyr	Ile	Pro
305					310					315					320
Pro	Gly	Gln	Arg	Asn	Arg	Glu	Val	Leu	Ser	Trp	Gly	Ser	Gly	Arg	Gln
			325						330					335	
Ser	Ser	Pro	Arg	Met	Gly	Gln	Pro	Gly	Pro	Gly	Ser	Met	Pro	Ser	Arg
			340					345					350		
Ala	Ala	Ser	His	Thr	Ser	Asp	Phe	Asn	Pro	Asn	Ala	Gly	Ser	Asp	Gln
	355						360					365			
Arg	Val	Val	Asn	Gly	Gly	Val	Pro	Trp	Pro	Ser	Pro	Cys	Pro	Ser	Pro
	370					375					380				
Ser	Ser	Arg	Pro	Pro	Ser	Arg	Tyr	Gln	Ser	Gly	Pro	Asn	Ser	Leu	Pro
385					390					395					400

Pro Arg Ala Ala Thr Pro Thr Arg Pro Arg Ala Glu Phe Leu Gln Pro  
405 410 415

Gly Asp